

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: JACOBSON, Myron K.; JACOBSON, Elaine L.; AMÉ, Jean-Christophe; LIN, Winston

(ii) TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG) ENZYMES, THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIVE THEREWITH

(iii) NUMBER OF SEQUENCES: 38

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fulbright & Jaworski L.L.P.
(B) STREET: 666 Fifth Avenue
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10103

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
(B) COMPUTER: IBM PS/2
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Concurrently Herewith

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: John E. Lynch
(B) REGISTRATION NUMBER: 20,940
(C) REFERENCE/DOCKET NUMBER: NIAD 201-JEL/ES

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 212-318-3000
(B) TELEFAX: 212-752-5958

(2) INFORMATION FOR SEQ ID NO: 1:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4069 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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1  accggaaggt gaacgaagcc cgaatcagaa cggtcatcc tgaggctggt aggggtgcgg
61  tggaagaggg aaggcaggcg tctggatagg gcctggttcg ggaggctgtc agagcaggag
121  ctgcagaagc agtcagcggc agagggggca tggtgccggg aggcaccgag gaggggggcg
181  agtcctgccc tcccagggtt agtgaatgag gctctacgcc cgggctggcc cgggagactca
241  gtgtgcggcg tcccagcatg agtgcgggcc cgggtgtgta gccctgcacc aagcgacccc
301  gctgggacgc cgctgcaact tctccgcggc cggcctcgga cggccggagc ttcccggca
361  ggcagaggcg cgtcctcgat tccaaggacg ctccggtgca gttcagggtc ccgccgtcct
421  cgtcaggctg cgccctgggc cgggcgggac agcaccgagg cagcggcacc tctcttgttt
481  tcaaacagaa gactataacc agttggatgg acactaaagg aatcaagaca gttgaatcag
541  aaagtgttga tagtaaagaa aacaacaata caagagaaga atccatgatg agttctgtac
601  aaaaagataa cttttatcaa cataacatgg aaaaattaga aaatgtttct cagctagggtt
661  ttgataagtc accagttgaa aaaggtacac agtatttgaa gcagcatcag actcggcta
721  tgtgtaagtg gcagaatgaa gggccacact cagaacggct tttggaaagt gaacctccag
781  cggtaactct ggtaccagag cagttcagta atgctaattg cgatcagtcg tcccaaagg
841  atgatcacag tgacacaaat agtgaggaga gtagagataa tcagcagttt ttgacacatg
901  taaagcttgc gaatgcaaag cagacgatgg aagatgaaca gggcagagaa gccagaagcc
961  accagaagtg tggcaaggct tgccatcctg cagaagcctg tgcagggtgt cagcaggagg
1021  agacagacgt ggtgtccgag agccccttgt cggacactgg ctctgaggat gttggtactg
1081  gactgaaaaa tgccaacaga ttgaatagac aagaaaagtag tctaggaaat tctcctocat
1141  ttgagaaaga aagtgaacct gagtcaccaa tggatgtaga taattccaaa aatagttgtc
1201  aggattcaga agcagatgaa gagacaagtc caggttttga tgaacaggaa gatagcagtt
1261  ctgctcaaac agcaataaaa ctttcaaggc tccaaccaag agaagctgac actgagttga
1321  ggaagcggtc ctctgctaag ggaggtgaga ttcgattaca tttccaattt gaaggaggag
1381  agagtcgagc tggaaatgaa gatgtgaatg ccaaacgacc tggaaagtact tctagcctga
1441  atgtagagtg cagaaaattc aagcaacatg ggagaaaagga ttctaaaatc acagatcatt
1501  tcatgagagt gcccaaagca gaggacaaaa gaaaagaaca atgtgaaatg aaacatcaaa
1561  gaacagaaaag gaagatccct aaatacatto cacctcacct tctccagat aagaaatggc
1621  ttggaactcc tattgaggag atgaggagaa tgccaagggtg tgggatccgg ctgcctccct
1681  tgagaccatc tgccaatcac acagtgacta ttcggttaga tcttttgcca ataggagaag
1741  ttccataaac tttcccaaca cattttaaag atttgtggga caacaagcat gttaagatgc
1801  cttgttcaga acaaaaactt taccctgtgg aagatgagaa tggtgagcga gctgcaggca
1861  gccggtggga actcattcag actgcacttc tcaacaggct cactcggccc cagaacctga
1921  aggatgctat tctgaagtac aatgtggcat attctaagaa atgggacttt acagctttga
1981  ttgattttct ggataaggta ctagaagaag cagaagctca acacttgat cagtccatct
2041  tgcttgatat ggtgaaaatt gcactctgtc tgccaaatat ttgtacccag ccaataccac
2101  tcctgaaaca gaagatgaat cattccatca caatgtcaca ggaacagatt gccagctttt
2161  tagctaattg tttcttctgc acgtttccac gacgcaatgc caagatgaaa tcagagtatt
2221  ccagttatcc agatattaac ttcaatcggc tgtttgaagg acgttcatca aggaaaccag
2281  agaagcttaa aacgctcttc tgctacttta gaagagtcac agagaaaaaa cccactgggt
2341  tggtgacatt cacaagacag agtcttgaag attttccaga gtgggaaaga tgtgaaaaac
2401  tcctgactcg actgcatgtc acttacgaag gtacataga aggaaacggc cagggcacgc
2461  tacaggtgga ttttgcaaac cgtttcgttg gaggtggtgt aaccagtgcg ggacttgtc
2521  aagaagaaat ccgcttttta atcaaccctg agttgattgt ttacaggctc ttactgagg
2581  tgctggatca caatgaatgt cttatcatca caggactga gcagtacagt gaatacacag
2641  gctatgccga aacataccgc tgggcccggg gccatgaaga caggagcgaa agggacgact
2701  ggcagaggcg cagcactgag atcgtcgcca tcgacgcctt ccacttcaga cgctacctcg
2761  accagtttgt gcccgagaag atcagacggg agcttaacaa ggcttactgt ggattttctc
2821  gtccctggag ttctcagag aacctgtctg cagtggctac aggaaactgg ggtgtggtg
2881  cctttggggg tgatgctaga ctaaaagcct taatacagat cctggcagct gctgtgctg
2941  agcgagacgt ggtttatttc acctttgggg actcagaact gatgagagac atttacagca
3001  tgcatatact cctcactgag aggaaactga ctgttgagaa agtatataag ctgctgtcac
3061  gatattacaa tgaagaatgc agaaaactgt ccacccccgg accagacato aagctttatc

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3121 cattcatata ccatgcagtt gagtcctgta cacagaccac caaccagccg ggacaaagga
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3241 gtgtgaactg acatgatatc catgtgtata taatccgcgt ttgtaggcaa ggatgcagtc
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3661 aaataatata gatctcctag gttaagagtt ttatatatta gaatactttt caaaaagtta
3721 ttttgagata tcacctttat ttgtaatggt aatttgccctg tcccttttcc cctgatcaat
3781 ttgtattgac tgttttttga aattgaccca aatgaaagga aatatgagaa taagagtttc
3841 ccaaattggtg tttaaaaaca aacaggttca agacacgcga aggacctcgt ttctctgggat
3901 tttttttctt tttctttttt tgaattagga ttattgtttg ttccttggtg cttgagacat
3961 attcatataa ccaaagttaa ggaactggga acttcgtggt gatttgatac tattgaagtt
4021 totctggtac tcaaaggtta tgtagttaat aaattttcat taacaaaaaa

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 977 amino acids

(B) TYPE: protein

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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1 MSAGPGCEPC TKRPRWDAAA TSPPAASDAR SFPGRQRRVL DSKDAPVQFR VPPSSSGCAL
61 GRAGQHRGSA TSLVFKQKTI TSWMDTKGIK TVESESLHSK ENNNTREESM MSSVQKDNFY
121 QHNMEKLENV SQLGFDKSPV EKGTYLQKH QTAAMCKWQN EGPHERLLE SEPPAVTLVP
181 EQFSNANVDQ SSPKDDHSDT NSEESRDNQ FLTHVKLANA KQTMEDQGR EARSHQKCGK
241 ACHPAEACAG CQEEETDVVS ESPLSDTGSE DVGTLKLAN RLNRQESSLG NSPPFEKESE
301 PESPMVDNS KNSCQDSEAD EETSPGFDEQ EDSSSAQTAN KPSRFQPREA DTELKRSSA
361 KGGEIRLHFQ FEGGESRAGM NDVNAKRPGS TSSLNVECRN SKQHGRKDSK ITDHFMVRVPK
421 AEDKRKEQCE MKHQTERKI PKYIPPHLSP DKKWLGTPIE EMRRMPCGI RLPPLRPSAN
481 HTVTIRVDLL RIGEVKPFEP THFKDLWDNK HVKMPCEQN LYPVEDENGE RAAGSRWELI
541 QTALLNRLTR PQNLKDAILK YNVAYSKKWD FTALIDFWDK VLEEAEQHL YQSILPDMVK
601 IALCLPNICT QPIPLLKQKM NHSITMSQEQ IASLLANAF CTFPRRNAKM KSEYSSYPDI
661 NFNRLFEGRS SRKPEKLKTL FCYFRRVTEK KPTGLVTFTR QSLEDFPEWE RCEKLLTRLH
721 VTYEGTIEGN QGQMLQVDF NRVFVGGVTS AGLVQEEIRF LINPELIVSR LFTEVLHDNE
781 CLITGTQEQY SEYTGAEY RWARSHEDRS ERDDWQRRT EIVAILDHF RRYLDQFVPE
841 KIRRELNKAY CGFLRPGVSS ENLSAVATGN WCGAFGGDA RLKALIQILA AAVAERDVVY
901 FTFGDSELMR DIYSMTFLT ERKLTVEGVY KLLRLRYNEE CRNCSTPGPD IKLYPFIYHA
961 VESCTQTTNQ PGQRTGA

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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4069 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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1 ggcgtctggg aagtgaggag cgtctctgcc tggcagaggc tgcaatctct gcactttggg
61 gggccaaggc aggcgctgag aaggacgcgc agtccatctc totcaggtta gtgaaatgag
121 gctctccgcg gggccggccc ggggacagtg cgctgctggt cccagcatga atgccccccc
181 cggctgtgaa ccctgcacca aagcgaccgc ctggggcgcc gctacaactt cgcggctgc
241 ttcggacgcc cggagcttcc cgagcaggca gaggcgctc ctgcacccca aggacgctca
301 cgtgcagttc agggctccac cgtctctgcc agcctgcgtc ccagggcagg cgggacagca

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361 cagaggcagc gccacctcgc ttgttttcaa acaaaagact attaccagtt ggatggacac
421 taaaggaatc aagacagcgg aatcagaaa tttggatagt aaagaaaaca acaatacaag
481 aatagaatcc atgatgagtt ctgtacaaaa agataacttt taccaacata atgtagaaaa
541 attagtaaat gtttctcagc taagtcttga taagtcactc actgaaaaaa gtacacagta
601 tttgaaccag catcagactg cagcaatgtg taagtggcaa aatgaaggga aacacacgga
661 gcagcttttg gaaagtgaac ctcaaacagt aaccctggta ccagagcagt ttagtaatgc
721 taacattgat cggtcacctc aaaatgatga tcacagtgac acagatagtg aagagaatag
781 agacaatcaa cagttttctc caactgtaaa gcttgcaaat gcaaagcaga ctacggaaga
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2521 tactgagcag tacagtgaat acacaggcta tatogttggg cccggagcca
2581 cgaagatggg agtgaaaggg acgactgcga actgagatcg ttgccatcga
2641 tgctcttcac ttccagacgt accctcgata gagaaaatga gacgcgagct
2701 gaacaaggct tactgtggat ttctocgtcc tgagatttct tcagagaatc tttctgcagt
2761 ggccacagga aactggggct gtgggtgcct gccaggttaa aagccttaat
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2881 agaattgatg agagacattt acagcatgca cttttcctt actgaaagga aactcactgt
2941 tggagatgtg tataagctgt tgctacgata ctacaatgaa aactgtccac
3001 cctggacca gacatcaagc tttatccatt catataccat gctgtcagat cctgtgcaga
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3181 aagttaatat aaatgtgtac ataatccaca tttgtagtca aggaacgaat ctcttccaca
3241 catgtgcagt tgtcagttgg tacatctaaa ctccctocat cctgactcac gtggacttag
3301 atatgttttg tttctatttt cttctatttt agtttttcat tctttgatgt ttatttcttt
3361 tgtccatcag atctcttgtg aaatcccatg cttactgctt ctcagctgtc ggggtctctt
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3601 taattagggt tttttcata tgtgttgcac aatgcaaacc tcttaggtta aaatagtttc
3661 tttattttaag atagaataat ttccagaaat tgtacttttg aggtatcatt tttatctgta
3721 atggtttgtc tgtctttttt cctctgatca gtattttttt ataccagttt tggagactgc
3781 ctgagatgaa aggaaatgtg gaataaaaag aggttttctt gatgtggtg gaagaaaaca
3841 gattccaaga gaattgaaga ttttttttgt ttcttggta ctttttctt tttaaattag
3901 gactaatgtt tcttttgtgg tgcttgaggc atattcatat aaccaagtt tgagaactgg
3961 gaacttoatg ctgatttgta catattgaag tttctctggt attcaaaggt tatatagtga
4021 atgaattttc attaataaat cactttgtca gaaaaaaaa aaaaaaaaa

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 amino acids
- (B) TYPE: protein
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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1   MNAGPGCEPC TKATRWAAT TSPAASDARS FPSRQRRVLD PKDAHVQFRV PPSSPACVPG
61  QAGQHRGSAT SLVFKQKTIT SWMDTKGIKT AESESLDSKE NNNTRIESMM SSVQKDNFYQ
121 HNVEKLVNVS QLSLDKSLTE KSTQYLNQHQ TAAMCKWQNE GKHTEQLLS EPQTVTLVPE
181 QFSNANIDRS PQNDHSDTD SEENRDNQOF LTTVKLANAK QTTEDEHARE AKSHQKCSKS
241 CHPGEDCASC QQDEIDVVPK SPLSDVGSSE VGTGSKNDNK LIRQESCLGN SPPFEKESEP
301 ESPMDVDNSK NSCQDSEADE ETSPGFDEQE DGSSSQTANK PSRFQARDAD IEFKRKYSTK
361 GGEVRLHFQF EGGESRTGMN DLNAKLPGNI SSLNVECRNS KQHGKKDSKI TDHLMRLPKA
421 EDRRKEQWET KHQRTERKIP KYVPPHLSPE KKWLGTPIEE MRRMPRCGIR LPLLRPANH
481 TVTIRVDLLR AGEVPKPFPT HYKDLWDNKH VKMPCSEQNL YPVEDENGER TAGSRWELIQ
541 TALLNKFTTRP QNLKDAILKY NVAYSKKWDF TALIDFWDKV LEEAEAQHLY QSILPDMVKI
601 ALCLPNICTQ PIPLLKQKMN HSITMSQEIQ ASLLANAFFC TFPRRNAMKM SEYSSYPDIN
661 FNRLFEGRSS RKPEKLKTLF CYFRRVTEKK PTGLVTFTRQ SLEDFPEWER CEKPLTRLHV
721 TYEGTIEENG QGMLQVDFAN RFVGGGVTS A GLVQEEIRFL INPELIISRL FTEVLHDNEC
781 LIITGTEQYS EYTGYAETIR WSRSHEDGSE RDDCERRCTE IVIDALHFR RYLDQFVPEK
841 MRRELNKAYC GFLRPGVSSE NLSAVATGNW GCGAFGGDAR LKALIQILAA AAAERDVVYF
901 TFGDSELMRD IYSMHIFLTE RKLTVGDVYK LLLRYYNEEC RNCSTPGPDI KLYPFIYHAV
961 ESCAETADHS GQRTGT

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(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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1   ggggggactgt gtgctgcggg tcccagcatg agtgcggggcc ccggtcgagg gcoctgcacg
61  aaagcgcgct ggggcgcgcg tggaaacttct ggcgcgactg cctcggaact ccggagcttc
121 cctggcaggc agaggcgtgt tctcgacccc aaggacgctc ccgtccagtt cagggtccct
181 ccgtccctgc cagcctgcgt ctccggggcg gcgggaccgc acagaggcaa cgcacactcg
241 tttgttttca aacaaaagac tattactact tggatggata ctaaaggacc caagacagct
301 gaatcagaaa gtaaagaaaa caacaatata agaattgact ccatgatgag ttctgtgcag
361 aaagataact tttaccaca taaggtggaa aaattggaaa atgttccctc gctaaatctt
421 gataaatcac ccacagaaaa gagttcacag tatttgaacc aacagcagac tgcgagtgtg
481 tgcaagtggc agaataaggg gaagcatgca gaacagcttt tggcaagtga gcctcccgcg
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661 aaacttgcaa atacaaagcc aacagtagga gatgggcagg ccagaagcaa ctgtaagtgc
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901 agtgagcctg agtcaccaat ggatgtagac aactcgagaa acagttgtca agattcagaa
961 gcagatgaag aaacaagtcc agtctttgat gagcaagatg atcgttcctc ccaaacagca
1021 aataaaacttt caagttgcca agcaagagaa gctgatggcg atcttaggaa acggtatttg
1081 actaagggaa gtgaagttag attgcatttc caattgaaag gagaaaataa tgctgggacc
1141 agtgacttaa atgccaaagg atctggaaac tcttctagcc ttaatgtaga gtgtgaagat
1201 tccaagcagc atggaaaaag ggattctaaa attacagatc atttcatgag aatttccaag
1261 tcagaggaca gaagaaaaga acaatgtgaa gtcagacatc aaagaacaga aaggaagatt
1321 ccaaaaatata tcccacctaa cctccctcca gagaagaagt ggctgggaac tcctatttag

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1381 gaaatgagaa aaatgcctcg gtgtgggac catttgccct cottaagacc atctgcaagt
1441 cacacagtga ctgttcgggt agaccttctg agagcaggag aggttcgaa accttttcca
1501 acacattaca aagatttgtg ggataacaaa catgtgaaaa tgccttggtc ggaacaaaaa
1561 ttgtaccctg tggagatga gaatggtgag cgaactgcag ggagtaggtg ggagctcatt
1621 cagactgcac ttctcaacaa attcacacga cccagaaact tgaaggatgc gattctgaaa
1681 tacaatgtgg catattctaa gaaatgggac ttacagcctt tgggtgattt ctgggataag
1741 gtacttgaag aagcagaggc ccaacattta tatcagtcca ttttacctga catggtgaaa
1801 attgcactct gtctgccaaa tatttgacc cagccaatac cactcctgaa acagaagatg
1861 aatcattctg tcacgatgtc acaggaacag atcgccagtc ttttagctaa tgctttcttc
1921 tgcacatttc cccgacggaa tgccaagatg aaatcggagt attctagtta ccagacattt
1981 aacttcaatc ggttgtttga aggacgttca tcaaggaaac cagaaaaact gaaaaactc
2041 ttctgtact ttcaagagt cacagagaaa aaacctacag gattggtgac atttacaaga
2101 cagagtcttg aagattttcc agaatgggaa aggtgtgaaa agcctctgac acgcttacac
2161 gtcacttacg agggatccat agaaggcaac ggccgaggca tgctacaggt ggattttgca
2221 aatcggtttg ttggaggtgg tgtgactggt gcgggacttg tacaagaaga aatcagattt
2281 ttaatcaatc tcgaattgat tgtttcacgg ctgttcactg aggtgctgga tcacaatgag
2341 tgtcttatta tcacaggtac tgaacagtac agtgaataca caggctatgc tgaacttat
2401 cgttggggccc gaagccatga agatgggagt gaaaaggacg attggcagcg gcgctgcacg
2461 gagatcggtg ccattgacgc acttcacttc agacgctacc togatcagtt tgtgcctgag
2521 aaagtgaagc gtgagcttaa caaggcttac tgcggattcc tccgtcctgg agttccttct
2581 gaaaaatctt ctgcagtggc caggggaaac tggggctgtg gtgccttttg gggtagcgt
2641 agattaaaag ccttaataca gatcctggca gctgctgcgg ctgaacgtga cgtggtttat
2701 ttcaccttgg gggactcaga gttgatgaga gacatttaca gcatgcacac tttccttacc
2761 gagaggaagc tggatgttgg aaaagtgtac aagttattgc ttagatacta caatgaagaa
2821 tgcagaaact gttccacccc tggaccagac atcaagcttt atccattcat ataccatgct
2881 gttgagtcaa gtgcagagac cactgacatg ccaggacaga aggcaggcac ctgaggaaca
2941 agtgactagg acctcctctc aaagagacat cctatttgaa atgtggggtg tgatgtctga
3001 attgactgaa tctgatctaa gtgtgtatat aatccacatt tgtaatcaag gatgcagttc
3061 cttctgcata tgcagttggt tcttgttcat cctggtggac atgcctttag acatggcttc
3121 ttcaattttt cttctccttc agtctttatt ctttgatttt ttttttccaa cttgatttct
3181 tgggaaaact caagaaaggt tgcactcagc ttctagatct ttctcttctt gtctgtgtgt
3241 tgtccagact gctttggtgg ctagcagata ccacacact tggaggaagt tacaatcca
3301 gaaatctgag tttgctgcag atttacctgt gagcttctca ctcccaaccc ttgttaggct
3361 tgtgttctct acattttcaa ttttggaggt tgaagttttt cttatgttac ttaatgctag
3421 tatcttttag gctaaaaacta ttttctattt aaggcagact aatttccagt ttctcttttg
3481 aaacatcatc cctataagta acggtttttt tcttctttt ttccccagcg ctattttaga
3541 agctggccaa gaggaagaa aatgtagaat aaaaggattt tctcgggatg ctataaagaa
3601 gccaggttca agagcgttgg ggtttttgtt tttttcaaga cttgtttttc ctttgcagct
3661 aggggtgagt cttgttctgt ggtgctgagg gcatagtcct gtaaccaaag gtctttgctg
3721 gagacttgat gctgatttgt acatattgaa gtttctctgg caggaaatat tagagttaat
3781 aaatttcatt aataaatcat ttgtcagaaa aaaa

```

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 968 amino acids

(B) TYPE: protein

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

1 MSAGPGWEPC TKARWGAAGT SAPTASDSRS FPGRQRRVLD PKDAPVQFRV PPSSPACVSG
61 RAGPHRG NAT SFVFKQKTIT TWMDTKGPKT AESESKENNN TRIDSMSSV QKDNFYPHKV
121 EKLENVQNLN LDKSPTEKSS QYLNQQQTAS VCKWQNEGKH AEQLLASEPP AGTPLPKQLS
181 NANIGQSPHT DDHSDTDHEE DRDNQQFLTP IKLANTKPTV GDGQARSNCK CSGSRQSVKD
241 CTGCQQEEVD VLPESPLSDV GAEDIGTGPK NDNKLTGQES SLGDSPPFEK ESEPEPMDV
301 DNSRNSCQDS EADEETSPVF DEQDDRSSQT ANKLSSCQAR EADGDLRKRY LTKGSEVRLH
361 FQFEGENNAG TSDLNAKPSG NSSSLNVECR SSKQHGRKDS KITDHFMRIS KSEDRRKEQC
421 EVRHQRTERK IPKYIPP NLP PEKKWLGTPI EEMRKMPRCG IHLPSLRPSA SHTVTVRVDL
481 LRAGEVPKPF PTHYKDLWDN KHVKMPCSEQ NLYPVEDENG ERTAGSRWEL IQTALLNKFT

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541	RPQNLKDAIL	KYNVAYSKKW	DFTALVDFWD	KVLEEAEAOH	LYQSILPDMV	KIALCLPNIC
601	TQPIPLLKQK	MNHSVTMSQE	QIASLLANAF	FCTFPRRNAK	MKSEYSSYPD	INFNRLFEGR
661	SSRKPEKLKT	LFCYFRRVTE	KKPTGLVTF	RQSLDFPEW	ERCEKPLTRL	HVTYEGTIEG
721	NGRGLQVDF	ANRFVGGGVT	GAGLVQEEIR	FLINPELIVS	RLFTEVLDHN	ECLIITGTEQ
781	YSEYTGyaET	YRWARSHEDG	SEKDDWQRR	TEIVAIDALH	FRRYLDQFVP	EKVRRELNKA
841	YCGFLRPGVP	SENLSAVATG	NWGCgAFGGD	ARLKALIQIL	AAAAAERDVV	YFTFGDSELM
901	RDIYSMHTFL	TERKLDVGKV	YKLLLRYYNE	ECRNCSTPGP	DIKLYPFIYH	AVESSAETTD
961	MPGQKAGT					

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2781 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

1	tcgaagtgtg	tggattttat	aaagtgcgat	attcatcaca	gctatcgctc	atccccaaaa
61	caccggtatg	caagaattca	ggtcacacatt	gattttttcog	atattocaaa	aggtttacca
121	atctacggca	aatcgccgca	gagcaagtgc	atccgtgctg	accaatcgac	tcggcaaggc
181	tttgtgtctta	aactgcgcca	ggatgtcgaa	gtcgccggat	ggcgggattt	ccgaaataga
241	aacggaggag	gagccggaaa	atctggcgaa	ctccctagat	gattogtggc	gtggagtttc
301	catggaggct	atacatcgta	atcggcagcc	tttcgaattg	gagaatttgc	caccagtgc
361	tgcgggcaat	ctccaccggg	ttatgtacca	gctgccaatt	cgtgaaacac	cgccacgccc
421	ctacaaatca	cgggaaaagt	gggactccga	gcatgtgcgt	ctgccctgtg	cgcccagatc
481	gaaatatccg	agggagaatc	cggatggcag	caccaccatc	gattttcgct	gggaaatgat
541	cgaacgagcc	cttctgcagc	ccataaagac	gtgtgaggaa	ctgcaggcgg	cgataaatatc
601	atataatacc	acctataggg	atcagtggca	ctttcgtgcc	cttcacaaac	ttctcgacga
661	ggaactggac	gagagcgaaa	cacgggtttt	cttcgaggat	ctattgcgcg	gcattatccg
721	attggcattg	cggctaccgg	acttgattca	atcgccagtt	ccgctgtctc	agcaccacaa
781	gaacgcctca	ttgagcctga	gccaaacagca	gatctcctgc	ctgttgccca	atgccttctt
841	gtgcacgttt	ccccgaagaa	acaccctcaa	gaggaagtcc	gagtaacagca	cttttccaga
901	catcaacttt	aacaggcttt	accaatcgac	gggaccggca	gttctggaga	agcttaaatg
961	cattatgcac	tatttttcgtc	gcgtgtgtcc	cacagagcgg	gatgccagca	atgtgcccac
1021	cggtgtggta	acctttgttc	gtcggagcgg	attgccggaa	catctgatcg	actggagcca
1081	aagtgcggcg	cgttggtgtg	atgtgccatt	gcacgtggat	gccgagggaa	caatcgagga
1141	tgagggcatt	ggactgctgc	aagttagactt	tgccaaacaaa	tatttggtgtg	gcggtgtctt
1201	gggacatggc	tgcgttcagg	aggagatacg	ctttgttatc	tgcccgagagc	tatttggtggg
1261	taaactcttt	acggagtgtc	tgcgaccatt	cgaggccctg	gtgatgttgg	gcgccgaaag
1321	gtatagtaac	tatacgggat	atgcgggaag	cttcgagtgg	tcgggcaact	ttgaggattc
1381	aacgccaaaga	gatagctcag	gtcgtcgaca	aacggccatt	gtggcaatcg	atgccctaca
1441	ttttgcccag	tcacatcatc	aatatcgca	ggatctcatg	gaaagggagc	tgaacaaggc
1501	gtacattgga	tttgttcaact	ggatgggtgac	gccgccaccg	ggtgtggcaa	ctggttaactg
1561	gggttgccgc	gcattcggcg	gtgactccta	tctgaaagcc	ctgctgcaac	ttatggtctg
1621	cgcccagttg	ggcagacctt	tggcctaacta	tacctttgga	aatgtggagt	ttagggatga
1681	ttttcatgaa	atgtggctgt	tgtttcgaaa	tgacgggact	acggtgcagc	agctttggag
1741	tatttttaagg	tcgtacagta	ggcttattaa	ggagaagagc	tccaaggagc	cgcgtgagaa
1801	taaggcatcc	aaaaagaagc	tatatgattt	tattaaagag	gaacttaaga	aggtcagaga
1861	tgtgcccggg	gaggagcat	ccgccgaagc	tggaaagctct	agagtagctg	gattaggcga
1921	aggaaaaatca	gaaacatcag	cgaaatcctc	gccagaactc	aaacaagcaac	ccgcccgacc
1981	gcaaatcacc	ataacgcaac	aaagtaccga	tctattgccc	gcgcaattat	cgcaagataa
2041	ctctaattct	tcggaagatc	aggcccttct	tatgctgtcg	gacgatgagg	aggccaatgc
2101	catgatggag	gocgctagtc	tggaggctaa	aagcagcgta	gaaataagca	acagcagcac
2161	aacgtccaaa	acgagcagta	cagccacgaa	atcaatgggt	tcagggtggcc	gccagttgag
2221	tctgctcgag	atgcttgaca	cccattatga	aaagggttcg	gcctogaaga	ggccacgaaa
2281	atcaccacaac	tgcagcaagg	ctgagggttc	agcaaagagt	cgtaaggaga	tcgatgtgac
2341	cgacaaggac	gaaaaggacg	atattgttga	ctaggtgata	ttgcactaca	ggattgttac
2401	tgcccccaaa	aattgaagag	gtataaaatg	tattgtagat	aactttaagg	acatatttag
2461	ggcatttttaa	agtaggatca	ttgtaagtgc	aataaagtga	aatttttttt	tttttttaat

2521 tatactatttc taatctgcaa agacaatfff aotgttaaat ttgtataaca ttogaattaa
 2581 ttaatatatac ttgttatatc atgcaaatct agcttttatt atgcgaaatt ttagattaaa
 2641 gccagtaaag tttcttttta ttttaaccgaa accctttgtt tattttattt gaccacaaca
 2701 agaacatcaa caacaacaac caccgaaaaaa aagcgaatat atatttgttt gttcgtatat
 2761 atatatatat ctaagcagat c

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 amino acids
- (B) TYPE: protein
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

1 MQEFRSHLIF PIFQKVYQST ANRRRASASV LTNRLGKALC LNCARMSKSP DGGISEIETE
 61 EEPENLANSL DDSWRGVSME AIHRNRQPF E LENLPPV TAG NLHRVMYQLP IRET PPRPYK
 121 SPGKWDSEHV RLPAPESKY PRENP DGSTT IDFRWEMIER ALLQPIKTCE ELQAAIISYN
 181 TTYRDQWHFR ALHQLLDEEL DESETRVFFE DLLPRIIRLA LRLPD LIQSP VPLLKHHKNA
 241 SLSLSQQQIS CLLANAF LCT FPRRNTLKRK SEYSTFPDIN FNRLYQSTGP AVLEKLK CIM
 301 HYFRRVC PTE RDASNVP TG VTFVRRSGLP EHLIDWSQSA APLGDVPLHV DAEGTIEDEG
 361 IGLLQVDFAN KYLGGGV LGH GCVQE EIRFV ICPELLV GKL FTECLRPFEA LVMLGAERY S
 421 NYTGYAGSFE WSGNFEDSTP RDSSGRRQTA IVAIDALHFA QSHHQYREDL MERELNKAYI
 481 GFVHVWMTTP PGVATGNWGC GAFGGDSYLK ALLQLMVCAQ LGRPLAYYTF GNVEFRDDFH
 541 EMWLLFRNDG TTVQQLWSIL RSYSLIKEK SSKEPRENKA SKKKLYDFIK EELKKVRDVP
 601 GEGASAEAGS SRVAGLGEGK SETSAKSSPE LNKQPARPQI TITQQSTDLL PAQLSQD NSN
 661 SSEDQALLML SDDEEANAMM EAASLEAKSS VEISNSSTTS KTSSTATKSM GSGGRQLSLL
 721 EMLDTHYEKG SASKRPRKSP NCSKAEGSAK SRKEIDVTDK DEKDDIVD

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

1 ATGAGCAAGA AGTTTATCGA ACTGGGTGAT CCTGTCACTC AAGACGAGAA
 51 AGACTACGAA GACTATGTCG GAGTTGGTTT CGCGCATCAA GTCCCGACAA
 101 TGAAAAGGCG GAAGTTGACA GAACATGGAA ATACTACAGA ATCAAAAAGAA
 151 GATCCTGAAG AGCCAAAAAG CCGTGACGTA TTTGTCTCCT CGCAGTCAAG
 201 TGATGAGAGT CAAGAAGATT CGGCTGAAAA TCCGGAGATC GCTAAAGAAG
 251 TGTCAGAAAA TTGTGAAAAT CTGACAGAAA CTCTCAAAAT TTCTAATATT
 301 GAGAGTTTGG ACAATGTTAC TGAAAGATCT GAACACACTC TTGATAATCA
 351 CAAAAGTACT GAACCAATGG AAGAAGATGT AAACAACAAG TCCAATATTG
 401 ACGTTGCGAT TAATTCTGAC GAGGATGATG AACTTGTTCT GGAAGAGAAT
 451 AATAAAGAAA TGAGGGATGG AGAACAAGTA CAACAGTTGT CACAGGATTT
 501 ATTCGCTGAT GATCAAGAGC TAATTGAATA TCCAGGAATT ATGAAAGACA
 551 CTACAACTCA ACTGGATATA ACAGATTCTG AAGTGGAGAC TGCTCAAAAA
 601 ATGGAAATGA TTGAAGAAAC TGAAGCAGAT TCGACATTTG TAGGCGAGGA
 651 TTCAAAAGCT ACGAAAAGCT TGAGGACATC CAGTTCAAGT TTCCTGTCAA
 701 CTGTTTCAAC ATGCGAAGCC CTTGCAAAAG GACGAGCAAG AATGTATCAA
 751 AAAGAGTTGG AAAAGCATGT GATTGCATTT ACTGAGGGAA ATCTCACACT
 801 ACAACCAGAT TTGAACAAAG TTGATCCCGA CAGAACTAT CGATATTGTA
 851 CAATTCCGAA CTTTCCAGCT TCCCAAGGAA AACTTCGAGA AGATAATCGA
 901 TATGGCCCAA AAATCGTTTT GCCTCAAAGA TGGCGAGAAT TTGATTGAG
 951 GGGCCGTAGA AGAGACTCAT ATTTCTATTT CAAACGTAAG CTCGATGGAT

1001 ATTTGAAATG CTACAAAACA ACTGGATATT TTATGTTTGT TGGACTTTTG
 1051 CACAACATGT GGGAAATTTGA CCCAGACATC ACATATAAAC TGCCAGCACT
 1101 GGAAATGTAT TACAAAGAGA TGTCGGAACT TGTTGGTAGA GAAGAGGTTT
 1151 TGGAAAAATT TGCACGAGTT GCCCGCATCG CAAAAACTGC TGAAGATATT
 1201 CTGCCAGAGC GAATTTATCG TC~~TT~~TGTTGGT GACGTCGAAT CAGCTACCTT
 1251 GAGCCACAAG CAATGTGCTG CACTTGTTGC GAGAAATGTTT TTTGCCCGAC
 1301 CGGACAGTCC TTTCA~~GT~~TTTC TGCCGAATTC TCTCGTCTGA TAAATCTATT
 1351 TGTGTGGAGA AACTTAAATT CCTGTTC~~ACT~~ TATTTGACA AAATGTCAAT
 1401 GGATCCACCG GATGGTGCCG TCAGTTT~~TT~~AG ACTTACAAAA ATGGATAAAG
 1451 ATACGTTCAA CGAAGAGTGG AAAGATAAAA AATTACGTTC TCTTCCTGAA
 1501 GTTGAATTCT TTGATGAAAT GCTTATTGAA GACACAGCTC TCTGTACACA
 1551 AGTTGATTTT GCGAACGAAC ATCTTGGTGG CGGAGTTT~~TA~~ AATCATGGGT
 1601 CTGTT~~C~~AGGA GGAGATCCGT TTCTTGATGT GTCCAGAAAT GATGGTTGGA
 1651 ATGTTGTTGT GCGAGAAAA GAAACAAC~~TG~~ GAAGCGATT~~T~~ CAATTGTTGG
 1701 AGCTTACGTT TTCAGTTCTT ATACTGGTTA TGGTCATACT CTAAAAATGGG
 1751 CAGAACTTCA ACCAAATCAT TCTCGTCAGA ATACAAACGA ATTTCGAGAT
 1801 CGTTTTGGAC GTCTTCGGGT AGAAACTATT GCAATCGATG CAATTCTGTT
 1851 CAAAGGATCA AAATTAGATT GTCAGACGGA GCAGTTAAAC AAAGCAAATA
 1901 TCATTAGGGA AATGAAGAAA GCATCTATCG GATTCATGAG CCAGGGACCG
 1951 AAATTCACAA ATATTCCAAT TGTTACTGGA TGGTGGGGAT GTGGAGCATT
 2001 TAATGGGGAC AAGCCATGA AGTTCATAAT CCAAGTAATT GCTGCCGGAG
 2051 TCGCTGATCG TCCACTTCAT TTCTGTT~~CAT~~ TTGGAGAACC CGAGCTTGCC
 2101 GCAAAGTGCA AGAAAATTAT AGAACGAATG AAACAGAAGG ACGTAACACT
 2151 TGGTAAGTCA TGTTTTTCAA TCTTCAGTTG A

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 amino acids
- (B) TYPE: protein
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

1 MSKKFIELGD PVTQDEKDYE DYVGVGFAHQ VPTMKRRKLT EHGNTTESKE DPEEPKSRDV
 61 FVSSQSSDES QEDSAENPEI AKEVSENCEN LTETLKISNI ESLDNVTERS EHTLDNHKST
 121 EPMEEDVNNK SNIDVAINSD EDELVLLEN NKEMRDGEQV QQLSQDLFAD DQELIEYPGI
 181 MKDTTQLDI TDSEVETAQK MEMIEETead STFVGEDSKA TKTVRTSSSS FLSTVSTCEA
 241 PAKGRARMYQ KELEKHVIAF TEGNLTLPD LNKVDPDRNY RYCTIPNFPA SQGKLREDNR
 301 YGPKIVLPQR WREFDSRGRR RDSYFYFKRK LDGYLKC~~YKT~~ TGYFMFVGLL HNMWFD~~PDI~~
 361 TYKLPALEMY YKEMSELVGR EEVLEKFARV ARIAKTAEDI LPERIYRLVG DVESATLSHK
 421 QCAALVARMF FARPDSPFSF CRILSSDKSI CVEKLKFLFT YFDKMSMDPP DGAVSFRLTK
 481 MDKDTFNEEW KDKKLRLPE VEFFDEMLIE DTALCTQVDF ANEHLGGGV~~L~~ NHGSVQEEIR
 541 FLMCP~~EM~~VG MLLCEKMKQL EAISIVGAYV FSSYTG~~Y~~GHT LKWAELQPNH SRQNTNEFRD
 601 RFGRLRVETI AIDAILFKGS KLDCQTEQLN KANIIREMKK ASIGFMSQGP KFTNIPIVTG
 661 WWGCGAFNGD KPLKFIIQVI AAGVADRPLH FCSFGEPELA AKCKKIIERM KQKDVTLGKS
 721 CFSIFS

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: polypeptide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

LFTEVL~~DHNE~~ CLIITGTEQY SEYTG~~Y~~AETY R

- (2) INFORMATION FOR SEQ ID NO: 12:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: polypeptide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: protein fragment

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AYCGFLRPGV SSENLSAVAT GNXGCGAFG

- (2) INFORMATION FOR SEQ ID NO: 13:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: polypeptide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: protein fragment

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

FLINPELIVS R

- (2) INFORMATION FOR SEQ ID NO: 14:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: polypeptide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: protein fragment

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

IALXLPNIXT QPIPLL

- (2) INFORMATION FOR SEQ ID NO: 15:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: polypeptide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: protein fragment

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GAYCAYAAYG ARTGYTT

- (2) INFORMATION FOR SEQ ID NO: 16:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: polypeptide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: protein fragment
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CKRTANGTYT CNGCRTA

- (2) INFORMATION FOR SEQ ID NO: 17:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: oligonucleotide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATCATCACAG GTACTGAGCA GTAC

- (2) INFORMATION FOR SEQ ID NO: 18:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: oligonucleotide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCCTGTGTAT TCACTGTACT GCTC

- (2) INFORMATION FOR SEQ ID NO: 19:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: polypeptide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: polypeptide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

EDKRKEQCEM KHQRTKIP KYIPPH

- (2) INFORMATION FOR SEQ ID NO: 20:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: polypeptide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: polypeptide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

EDRRKEQWET KHQRTKIP KYVPPH

- (2) INFORMATION FOR SEQ ID NO: 21:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: polypeptide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: polypeptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

EDRRKEQCEV RHQRTKIP KYIPPN

(2) INFORMATION FOR SEQ ID NO: 22:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: polypeptide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: polypeptide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

HQVPTMKRRK LTEHGNTTES LLLKEDPPEP KS

(2) INFORMATION FOR SEQ ID NO: 23:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: polypeptide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: polypeptide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

EGKRKGDEVD GVDEVAKKKS KKEKDK

(2) INFORMATION FOR SEQ ID NO: 24:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: polypeptide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: polypeptide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

EGKRKGDEVD GTDEVAKKKS RKETDK

(2) INFORMATION FOR SEQ ID NO: 25:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: polypeptide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: polypeptide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

EGKRKGDEVD GIDEVTKKKS KKEKDK

(2) INFORMATION FOR SEQ ID NO: 26:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: polypeptide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: polypeptide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

EGKRKGEEVD GNVVAKKKS KEKEK

- (2) INFORMATION FOR SEQ ID NO: 27:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: polypeptide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: polypeptide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

EGKRKADEV D GHSAATKKKI KKEKEK

- (2) INFORMATION FOR SEQ ID NO: 28:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: polypeptide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: polypeptide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

EELPDTKRAK MELSDTNEEG EKKQR

- (2) INFORMATION FOR SEQ ID NO: 29:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: polypeptide
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: polypeptide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

EGVSSAKKAK IEKIDEEDAA SIKELTEKIK K

- (2) INFORMATION FOR SEQ ID NO: 30:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: oligonucleotide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GCTGCGGGTC TCGACGATGA GTGCGGGC

- (2) INFORMATION FOR SEQ ID NO: 31:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: oligonucleotide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GGGTCTAGAA TTCACTTGGC TCCTCAGGC

- (2) INFORMATION FOR SEQ ID NO: 32:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: oligonucleotide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CCGGAATTCG GGTTTTTTGT TAATGAAAAT TTATTAAC

- (2) INFORMATION FOR SEQ ID NO: 33:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: oligonucleotide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TCAGAGCAGA TGAACGAG CAGTCCAGG

- (2) INFORMATION FOR SEQ ID NO: 34:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: oligonucleotide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

1 CCAATTTGAA GGAGGAATTC CCGCCGCCAC CATGAATGAT GTGAATGCCA AACGACCTGG
61 A

- (2) INFORMATION FOR SEQ ID NO: 35:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: oligonucleotide

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

gaattcccgccg ccaccATG AA

- (2) INFORMATION FOR SEQ ID NO: 36:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 674 bases
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

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1   agaagaaaat ggccaaggca tgetacaggt ggatttttgca aatcgttttg ttggaggtgg
61  tgtaaccagt gcaggacttg tgcaagaaga aatccgcttt ttaatcaatc ctgagttgat
121 tatttcacgg ctcttcaactg aggtgcttga tcacaatgaa tgtctaatta tcacaggtac
181 tgagcagtac agtgaatata caggctatgc tgagacatat cgttgggtccc ggagccacga
241 agatgggagt gaaagggacg actgcgagcg gcgctgcact gagatcgttg ccatcgatgc
301 tcttcacttc agacgctacc togatcagtt tgtgcctgag aaaatgagac gcgagctgaa
361 caaggcttac tgtggatttc tccgtcctgg agtttcttca gagaatcttt ctgcagtggc
421 cacaggaaac tggggctgtg gtgccttttg ggggtgatgcc aggttaaaag ccttaatata
481 gatattggca gctgctgcag ctgagcgaga tgtggtttat ttcacctttg gggactcaga
541 attgatgaga gacatttaca gcatgcacat tttccttact gaaaggaaac tcactgttgg
601 agatgtgtat aagctgttgc tacgatacta caatgaagaa tgcagaaact gttccacccc
661 tggaccagac atca

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(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```

1   aaaaatagtt gtcaagactc agaagcagat gaggagacaa gtccagggtt tgatgaacaa
61  gaagatggta gttcctccca aacagcaaat aaaccttcaa ggttccaagc aagagacgct
121 gacattgaat ttaggaaacg gtactctact aaggcgcttg aagttagatt acatttccaa
181 tttgaaggag gagagagtcg

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(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

1   gatctcgaag taaaaactca cgcagaaaaga gtcctcctc ctttagcatg agaatccaac
61  tttgtaatga taacactggc aacatcaaca gtttgagaga aagcacgtgc ttgggcttca
121 caagcttgtc caatagaagc atccatcaca aaaacaacat tatctggtgt aactgcgttg
181 gaaacttgga gcatttcttc gaaaagtga gcttcttgct tgtgacgacc tgatgtatca
241 acaatgatga ttctgaacct ttcttgctgc aaaacaaata ttattaaacc atttttctgt
301 gataaattac cgtgaatttt tctactcctt cggcggaat ttttacgggg tcaatttcag
361 agtatgatcc atagaaggga atacgagctt ttgtggcatt ttgctttaat tgatcaaaag
421 ctccagcacg gaatgtatcg gcacagatca gacatgtttt ccatcctttt ctttggtagt
481 aatacgccat ctgaacttga aaagtgttga aaagtgttga gaagtttact aattaaaaaa
541 tataatgttt gatggtgtgt gagctttcta ttgtaattca tggaaogaac cttggtacaa
601 gtcgtagtgt taccggaacc ttgaagacca acaaacatga aaacgttgcg acgtcctttt
661 gttggtgtga aaggagttac accaggatcc acaagcttca gcagttcatt gaatactgtc
721 ttctgaatgt accgacgttt gtttgcctct ccgacgatct cttogaaatt aatcgctttt
781 ctgaaaatat ttattaaatt taaatcttaa atagcgtaaa aatttacttc acgtttgtct
841 taagttgctt tacaagacga atatgaacat cagattcaat aagagctgta cagacttctt
901 tcagcatcaa atccagctcc cctcatttga taacgggtgt ctgacggagc tttcogatcg
961 catttcggat tttccgcccc aaatcggcc aaccattttt gaactgaaat ttgaaatgct
1021 ttaatttggt taagcataga attaaacgcy ttttaaatcg agagcaocat aaaaacagtt
1081 tggagaaaaa tcgataattc ttgtaggaga ttcagtccct gtgggtttct tcggcttctt
1141 aatcattttt tgacgacata gtggtatttc acaatagggt ttttcaagac acaacagatt
1201 tttcaciaag agtagagaag aaatggaaaa ctgtagattt cttctcgaag agccgagaaa
1261 ggcaagggtat tggaaagtta aaaaggtaat gtttctttat tcttttttca aaacaataat

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1321 aaatggaaaa tatatatatta tagataacaa tttcagacag ttaaaatcac gtgaaaaatt
1381 caaatattcaa cacaaaaaatt gacgagtggg accccgttgt tgcgccttga agagtaacgc
1441 ttgcgcgtttt gacgattttta ttgacgcggt tctgggtgcat gcgggaaatt ttttattttc
1501 aacttttttct ctgttttgttt atcctttttt aattgaattc tcatgatttg aaagctttga
1561 aaaatatttat tttgctcaaa aacatgcgtt ttgtaaaaca ttgattagat tcaaggcaat
1621 taatggatttt ttgcacgttc caaaaaaaag gaaattcatt ttttgaaaat tttgataatt
1681 taataatgaa aaatgttcca tagattttatt caatgccatc cttctctata atctcgaact
1741 tccgcacacct tcaactgtgg tagaggtatt tgcaatacca tatagtcgta ataataaact
1801 ttagtgaaca aatccaagac atcagctctt gagtaaataga atgattttata aaaactgctg
1861 attttctcgt aggaagaaaag agaatacagct aataatccgt cgttgtctat tctgtcaggc
1921 cgcttaaatg ttaaaaaata aaaacgtttt aagctaattt tgtatgtcta gaaactctaa
1981 ctcaacaagca tttctgcata cgccggatta gttgggtttg caaaaagcga gtaatctaca
2041 aaagtgaatt tttgattcat ctctccattt tcacaaaacc aattttgtgg taogtatttc
2101 atatgatctt catccacttt ttttagttttt gaatgtattt gtgtgagttg tgtccagatt
2161 tgaataagat aacatctcag atccaacttg caattgaagc aagaacgacg gatattctgat
2221 ttttatatga ccttaaaactt tatacttttg tagtttcgtc ctacacgaaa atataatttg
2281 tataggatat tacatctcta ggttttatgtg gttcaatttg atcctgtctt ggaataataa
2341 cacacgcac cataaaatga tctacaaatc gttcaatttg atttttctcg tttcaaatcg
2401 atttccaatt cgtaaaagttt gcattcaact ctatcacaca ctctgaaaag cacaatattc
2461 caaaatatgt tagtgaatca ctatcacaca ctctgaaaag cacaatattc cacaatattc
2521 gttataaatg aacctcacga ttcattcatta aattttctctt ggagcccgca taactattgc
2581 tgcccaatta aagtatcagt ttcacgattt gcagttctat cattttccgat agcctcaaat
2641 aagattttaat cttaagcgag tgttctgac aatttaaata tttgatactc accgcaagtt
2701 tcttcgaaac ttgttcgaaa gctggaattt tagaatatcc ttcaaaaactt ttttctctgc
2761 cctcatcaag ccataataag ttttgatcag caatatattc gaataaatta gtctctgata
2821 aatctcgtat cacaatcttt ttttctactc taaagaatac aattttgata agaataataa
2881 taattataat tataatagtt cgtcgtcag ttgatgaaga ccacataatt agtttaattg
2941 caagctatgc aacttgttga atactaatag gacttagcaa atcttatctt gaacctttt
3001 cattcgaaag aaaaatgaga tcgaatctcg ttcaaactgt ggagtagtca gtttaagaaac
3061 ttgtttctag tttgtgagga gacactggag aacgtgaaag tattacccat acgcaatatt
3121 tttgcggcga aaaatacggg acccggtctc gacacgacag tttttaaaac ttgtaaatag
3181 gtatgtaaaa gaaaacttta attttaaacg tgttgtttcg gaattttcat cgttttgtca
3241 tagttattct acaataaatt atttatgaaa aaaaaactaa aatataacta taataacacc
3301 tgaatattaa caaatcgatc gaaaaaaaac tatgaaaaaa atggatgaaa attccgcagc
3361 aacgagagtt tgaaatttca gtattcttta aaggcttacc gatttcaata aatagtgaca
3421 ctgaaaattg tagtttttaa actagttggt tagtatcatc aaatattcaa tcttcaaaa
3481 attcctcaat attaacgtat tttctctaatt tgtcttcatt atctaaaaaa aagttgcaat
3541 atatttttcc aggcagaaat agactttcac aaaacacatc gacacttoga atgagcaaga
3601 agtttatcga actgggtgat cctgtcactc aagacgttag ttatagtttt tattacttga
3661 acattatcat ctttttacag gagaaagact acgaagacta tgtcggagtt ggtttcgcgc
3721 atcaagtccc gacaatgaaa aggcggaagt tgacagaaca tggaaatact acagaaatca
3781 aagaagatcc tgaagagcca aaaagccgtg acgtatttgt ctctcgcag tcaagtgatg
3841 agagtcaaga agattcggct gaaaatccgg agatcgctaa ctctcgcag tcaagtgatg
3901 aaaatctgac agaaaactctc aaaatttcta atattgagag tttggacaat gttactgaaa
3961 gatctgaaca cactcttgat aatcacaaaa gtactgaacc aatggaagaa gatgtaaaaa
4021 acaagtccaa tattgacgtt gcgattaatt ctgacgagga aatggaagaa gatgtaaaaa
4081 agaataataa agaaatgagg gatggagaac aagtacaaca ggtcaggaaa ttttacaagt
4141 gaatgaaata agttaatcac caaaatgaat aaggacattt cccatcagaa aggtctctcg
4201 aatttttaggt gtaatgttaa ttttttgctg tagtttttcc cattgtttga aatttttgcc
4261 aaaattagtt attgcatacc cttcatgttt ttgaagattg tttaggaatg agaaaaacatt
4321 ttggacgctt ttattattag gacaccaaac actttttggt gaaaaaacag ctcgtttaaa
4381 aaaagctttt tccaaaaaat gctgacgcaag gcttgtgaat tttcgttttc cctgattttt
4441 taaaatttct cctaaagttt tttgctaata tttttcgcta tcgcgtaatt tactagttaa
4501 tcaacaaaaa attttttttt tttcatagat tttttataag tttttgaaaa catagattta
4561 aaacttaaac ttaaattttg acaaggcgag aggaaaaaat taaaaattgc tgaacattca
4621 gatgccggtt accttatttt ttggttcaaaa atcccaatat tacgcgtctg ggttatagtc
4681 atttgccctt attaaattta ttggttccct tggaaaagta agttctggtt tgttttcagc
4741 ttatcacttc atcaaacgga aggaagggtt gattaaggaa agtaaacata ttttatgttg
4801 ttcttgtcac ttcctccatt tcgcaataat ataactcgag aaatatagaa ttttgttcga
4861 agttttcttt ttccttcaac atttttaata ttgttagtat taccagaaaa aatagaaaaa
4921 atcgaagaaa tttgcaaaaa agcagacgta gaggctacgt acttcttaag caccgccctt
4981 ttctttttaa tttgttcggt cgtaccgaga tccggtacct tattttacia cgttttctgt

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5041	tccaaaaata	ataatgtact	gcagttgtca	caggatttat	tcgtgatga	tcaagagcta
5101	attgaatatc	caggaattat	gaaagacact	acaactcaac	tgatataac	agattctgaa
5161	gtggagactg	ctcaaaaaat	ggaaatgatt	gaagaaactg	aagcagattc	gacatttgta
5221	ggcgaggatt	caaaagttag	acaaaatcat	tctgacaagg	attcctgcga	gcactcagtc
5281	aagagcgagt	cacggcaact	cgggtccaaa	ccatttctaa	ttagtaaact	ctcaaaaacc
5341	acaactaaat	agctttaaac	ctttgtaaat	tagctttatt	ttgctaatta	gcaatgattt
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5521	aaagtggcac	tactagtgac	gaagttgacg	cagattctca	gattaatttg	gtaagacaaa
5581	gaaaatataa	atttttattac	ccagatgcat	attttcatga	ttctgatgca	aaaaatacgg
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5821	ttcaaagacg	cacaccattt	tgcataatac	aaacatttgt	cgtgtcgaaa	ccgggtaccg
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6001	aggacgagca	agaatgtatc	aaaaagagtt	ggaaaagcat	gtgattgcat	ttactgaggg
6061	aaatctcaca	ctacaaccag	atttgaacaa	agttgatccc	gacagaaact	atcगतattg
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6301	actagaacaa	ccatggagaa	agaatgcaaa	aaattgaatt	ttaaaaacta	attttttaat
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6661	actcaaaatt	ttctgaaaac	gccaaatttc	ataatgaaac	ttcttgaaaa	ctcttcagca
6721	aaaagttatg	acggctcaaa	aaatggccta	aaattagtta	agattggaga	tttgaccgac
6781	ttgtcaattg	cgcagcggct	ggaaacaaat	ttttttgaaa	tcaccgtcaa	attttaagta
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7021	taactaattt	caggccattt	tttgagccgt	cataactttt	ttctaaaaag	ttttcaagaa
7081	gtttcattat	gaaattccgt	gttttccagac	aatttttagt	ctaataagga	aataaaaaaa
7141	attcagagtac	accaccttta	agaaaaattt	ggattttccgc	tacgctaatc	cacctttaat
7201	caaaaaatatt	tgaagttatt	caaagttaaa	gaattatat	ttcagagggg	ccgtagaaga
7261	gactcatatt	tctatttcaa	acgtaagctc	gatggatatt	tgaaatgcta	caaaacaact
7321	ggataatttta	tgtttggtgt	aagtttttga	aatacaattc	gtttgaagat	ttactctatt
7381	ttcagggact	tttgcaaac	atgtgggaat	ttgacccaga	catcacatat	aaactgccag
7441	cactggaat	gtattacaaa	gagatgtcgg	aacttgttgg	tagagaagag	gttttggaat
7501	aattttgcacg	agttgcocgc	atcgcaaaaa	ctgctgaaga	tattctgccca	gaggtatgat
7561	ttatgagata	tacagcattt	octctaatag	tattgcatat	aaacattttca	ctttgaggtt
7621	atatcttggg	ttatttttaa	aatatcaata	aatacaaaa	aatagaaaaa	tgataaaaaa
7681	acattttgtc	agttgataat	ttgggtatag	tattcattca	taatttgatt	tttttagcga
7741	atttatcgtc	ttgttggtga	cgtcgaatca	gctaccttga	gccacaagca	atgtgctgca
7801	cttgtttgca	gaatgttttt	tgcccgacgc	gacagtcctt	tcagttttctg	ccggtgagta
7861	atacaagaat	gctcatattt	ttagaatcaa	tatttgcgaag	gaactttaat	cttacgtacg
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8161	cgtctgataa	atctatttgt	gtggagaaa	ttaaattcct	gttcaacttat	ttcgacaaaa
8221	tgtcaattgga	tccacccgat	ggtgcocgta	gttttagact	tacaaaaatg	gataaagata
8281	cgttcaacga	agatgggaaa	gataaaaaat	tacgttctct	tctgaagtt	gaattctttg
8341	atgaaatgct	tattgaagac	acagctctct	gtacacaagt	tgatttttgcg	aacgaacatc
8401	ttgggtggcg	agttttaaat	catgggtctg	ttcaggtagt	tattttaaagg	aatataagaa
8461	tttgaagttt	tatttttttt	atgcaggagg	agatccgttt	cttgatgtgt	ccagaaatga</

8761	caatcgaatgc	aattctgttc	aaaggatcaa	aattagattg	tcagacggag	cagttaaaca
8821	aagcaaatat	cattagggaa	atgaagaaag	catctatcgg	attcatgagc	cagggaccga
8881	aattcacaaa	tattccaatt	gttactggat	ggtggggatg	tgagagcattt	aatggggaca
8941	agccactgaa	gtgtatgtta	tttcattcgt	taaatattga	agatggagga	gagtgaatgg
9001	ggatttttgc	tcttttgcaa	aatggcctcc	ctatgtacct	gaaaaaaaaa	tgaaaaaatc
9061	gagaaatatt	gaaaacccaa	caacgaattt	ttcacaattt	tgccataaatt	tttgaatttt
9121	cgccaaaatc	ggaatcagcg	attcgcctcc	cccatttttc	cgccaatcat	ttataatgtg
9181	cggagctcaa	aaacactgat	tggctagaaa	gtgggcgtag	cttcttattt	cggaggaaat
9241	tcaaataggg	aagttaatct	aaattaaaac	aatctcgtta	aaaaatgttt	cttttttcaa
9301	tcttccttat	ttgtttaaat	ttttcttttt	aaagatcgto	taaaagctac	cagtatctga
9361	ttcaattatc	ggtttttttc	agtcataatc	caagtaattg	ctgccggagt	cgctgatcgt
9421	ccacttcatt	tctgttcatt	tggagaaccc	gagcttgccg	caaagtgcaa	gaaaattata
9481	gaacgaatga	aacagaagga	cgtaacactt	ggtaagtcac	gtttttcaat	cttcagttga
9541	tttgaaaaag	ttgtatcgag	ttggaaacag	cttttaatct	aaattctgct	aacttacagg
9601	catgctattc	agtatgataa	acaacacccg	cttgccacat	aagcactttg	cttttttcaa
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